1647

RAW SEQUENCE LISTING DATE: 03/28/2002
PATENT APPLICATION: **US/09/903,180B** TIME: 10:51:04

Input Set : **N:\Crf3\03192002\I903180.raw**
Output Set: **N:\CRF3\03282002\I903180B.raw**


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 1 <110> APPLICANT: De Robertis, Edward M.
 2       Bouwmeester, Tewis
 3 <120> TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 4       Factors
 5 <130> FILE REFERENCE: 510015-256
 6 <140> CURRENT APPLICATION NUMBER: US/09/903,180B
 7 <141> CURRENT FILING DATE: 2001-07-11
 8 <150> PRIOR APPLICATION NUMBER: US 60/020,150
 9 <151> PRIOR FILING DATE: 1996-06-20
10 <160> NUMBER OF SEQ ID NOS: 10
11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 270
15 <212> TYPE: PRT
16 <213> ORGANISM: Xenopus
17 <400> SEQUENCE: 1
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19         1               5                  10                  15
20        Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
21                    20                  25                  30
22        Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
23                35                  40                  45
24        Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
25            50                  55                  60
26        Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
27        65                  70                  75                  80
28        Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
29                        85                  90                  95
30        Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
31                    100                 105                 110
32        Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
33                115                 120                 125
34        Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
35            130                 135                 140
36        Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
37        145                 150                 155                 160
38        Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
39                        165                 170                 175
40        Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
41                    180                 185                 190
42        Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
43                195                 200                 205
44        Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
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45            210                 215                 220
46        Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
47        225                 230                 235                 240
48        Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
49                        245                 250                 255
50        Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
51                    260                 265                 270
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 1338
55 <212> TYPE: DNA
56 <213> ORGANISM: Xenopus
57 <400> SEQUENCE: 2
58        gaattcccag caagtcgctc agaaacactg cagggtctag atatcataca atgttactaa      60
59        atgtactcag gatctgtatt atcgtctgcc ttgtgaatga tggagcagga aaacactcag     120
60        aaggacgaga aaggacaaaa acatattcac ttaacagcag aggttacttc agaaaagaaa     180
61        gaggagcacg taggagcaag attctgctgg tgaatactaa aggtcttgat gaaccccaca     240
62        ttgggcatgg tgattttcgc ttagtagctg aactatttga ttccaccaga acacatacaa     300
63        acagaaaaga gccagacatg aacaaagtca agcttttctc aacagttgcc catggaaaca     360
64        aaagtgcaag aagaaaagct tacaatggtt ctagaaggaa tatttttcct cgccgttctt     420
65        ttgataaaag aaatacagag gttactgaaa agcctggtgc caagatgttc tggaacaatt     480
66        ttttggttaa aatgaatgga gccccacaga atacaagcca tggcagtaaa gcacaggaaa     540
67        taatgaaaga agcttgcaaa accttgtttt tcactcagaa tattgtacat gaaaactgtg     600
68        acaggatggt gatacagaac aatctgtgct ttggtaaatg catctctctc catgttccaa     660
69        atcagcaaga tcgacgaaat acttgttccc attgcttgcc gtccaaattt accctgaacc     720
70        acctgacgct gaattgtact ggatctaaga atgtagtaaa ggttgtcatg atggtagagg     780
71        aatgcacgtg tgaagctcat aagagcaact tccaccaaac tgcacagttt aacatggata     840
72        catctactac cctgcaccat taaaggactg ccatacagta tggaaatgcc cttttgttgg     900
73        aatatttgtt acatactatg catctaaagc attatgttgc cttctatttc atataaccac     960
74        atggaataag gattgtatga attataatta acaaatggca ttttgtgtaa catgcaagat    1020
75        ctctgttcca tcagttgcaa gataaaaggc aatatttgtt tgacttttt tctacaaaat    1080
76        gaatacccaa atatatgata agataatggg gtcaaaactg ttaaggggta atgtaataat    1140
77        agggactaag tttgcccagg agcagtgacc cataacaacc aatcagcagg tatgatttac    1200
78        tggtcacctg tttaaaagca aacatcttat tggttgctat gggttactgc ttctgggcaa    1260
79        aatgtgtgcc tcataggggg gttagtgtgt tgtgtactga ataaattgta tttatttcat    1320
80        tgttacaaaa aaaaaaaa                                                 1338
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 318
84 <212> TYPE: PRT
85 <213> ORGANISM: Xenopus frazzled
86 <400> SEQUENCE: 3
87        Met Ser Arg Thr Arg Lys Val Asp Ser Leu Leu Leu Leu Ala Ile Pro
88         1               5                  10                  15
89        Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
90                    20                  25                  30
91        Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
92                35                  40                  45
93        Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
94            50                  55                  60
95        Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
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96        65                  70                  75                  80
97        Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
98                        85                  90                  95
99        Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
100                   100                 105                 110
101        Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
102                115                 120                 125
103        Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
104            130                 135                 140
105        Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
106        145                 150                 155                 160
107        Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
108                        165                 170                 175
109        His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
110                   180                 185                 190
111        Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
112                195                 200                 205
113        Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
114            210                 215                 220
115        Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
116        225                 230                 235                 240
117        Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
118                        245                 250                 255
119        Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
120                   260                 265                 270
121        Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
122                275                 280                 285
123        Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
124            290                 295                 300
125        Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
126        305                 310                 315
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 1875
130 <212> TYPE: DNA
131 <213> ORGANISM: Xenopus frazzled
132 <400> SEQUENCE: 4
133        gaattccctt tcacacagga ctcctggcag aggtgaatgg ttagccctat ggatttggtt      60
134        tgttgatttt gacacatgat tgattgcttt cagataggat tgaaggactt ggatttttat     120
135        ctaattctgc acttttaaat tatctgagta attgttcatt ttgtattgga tgggactaaa     180
136        gataaactta actccttgct tttgacttgc ccataaacta taaggtgggg tgagttgtag     240
137        ttgcttttac atgtgcccag attttccctg tattccctgt attccctcta aagtaagcct     300
138        acacatacag gttgggcaga ataacaatgt ctcgaacaag gaaagtggac tcattactgc     360
139        tactggccat acctggactg gcgcttctct tattacccaa tgcttactgt gcttcgtgtg     420
140        agcctgtgcg gatccccatg tgcaaatcta tgccatggaa catgaccaag atgcccaacc     480
141        atctccacca cagcactcaa gccaatgcca tcctggcaat tgaacagttt gaaggtttgc     540
142        tgaccactga atgtagccag gacctttgt tctttctgtg tgccatgtat gcccccattt     600
143        gtaccatcga tttccagcat gaaccaatta agccttgcaa gtccgtgtgc gaaagggcca     660
144        gggccggctg tgagcccatt ctcataaagt accggcacac ttggccagag agcctggcat     720
145        gtgaagagct gcccgtatat gacagaggag tctgcatctc cccagaggct atcgtcacag     780
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146        tggaacaagg aacagattca atgccagact tctccatgga ttcaaacaat ggaaattgcg     840
147        gaagcggcag ggagcactgt aaatgcaagc ccatgaaggc aacccaaaag acgtatctca     900
148        agaataatta caattatgta atcagagcaa aagtgaaaga ggtgaaagtg aaatgccacg     960
149        acgcaacagc aattgtggaa gtaaaggaga ttctcaagtc ttccctagtg aacattccta    1020
150        aagacacagt gacactgtac accaactcag gctgcttgtg cccccagctt gttgccaatg    1080
151        aggaatacat aattatgggc tatgaagaca aagagcgtac caggcttcta ctagtggaag    1140
152        gatccttggc cgaaaaatgg agagatcgtc ttgctaagaa agtcaagcgc tgggatcaaa    1200
153        agcttcgacg tcccaggaaa agcaaagacc ccgtggctcc aattcccaac aaaaacagca    1260
154        attccagaca agcgcgtagt tagactaacg gaaaggtgta tggaaactct atggactttg    1320
155        aaactaagat ttgcattgtt ggaagagcaa aaaagaaatt gcactacagc acgttatatt    1380
156        ctattgttta ctacaagaag ctggtttagt tgattgtagt tctcctttcc ttctttttt     1440
157        ttataactat atttgcacgt gttcccaggc aattgtttta ttcaacttcc agtgacagag    1500
158        cagtgactga atgtctcagc ctaaagaagc tcaattcatt tctgatcaac taatggtgac    1560
159        aagtgtttga tacttgggga aagtgaacta attgcaatgg taaatcagag aaaagttgac    1620
160        caatgttgct tttcctgtag atgaacaagt gagagatcac atttaaatga tgatcacttt    1680
161        ccatttaata ctttcagcag ttttagttag atgacatgta ggatgcacct aaatctaaat    1740
162        attttatcat aaatgaagag ctggtttaga ctgtatggtc actgttggga aggtaaatgc    1800
163        ctactttgtc aattctgttt taaaaattgc ctaaataaat attaagtcct aaataaaaaa    1860
164        aaaaaaaaaa aaaaa                                                     1875
166 <210> SEQ ID NO: 5
167 <211> LENGTH: 896
168 <212> TYPE: PRT
169 <213> ORGANISM: Xenopus
170 <400> SEQUENCE: 5
171        Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
172         1               5                  10                  15
173        Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu
174                    20                  25                  30
175        Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
176                35                  40                  45
177        Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
178            50                  55                  60
179        Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
180        65                  70                  75                  80
181        Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
182                        85                  90                  95
183        Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
184                    100                 105                 110
185        Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
186                115                 120                 125
187        Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
188            130                 135                 140
189        Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
190        145                 150                 155                 160
191        Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
192                        165                 170                 175
193        Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
194                    180                 185                 190
195        Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
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